Method andmaterials: We were observed 316 (male) student, who arrived from all province of Mongolia in Ulaanbaatar. They are divided into 4 groups by date of birth: 1. Born before 1987; 2. Born in 1988–89; 3. Born in 1990; 4. Born after 1991 (after launching HBV vaccination), In all serum samples tested for HBsAg, anti-HBc and anti-HBs by ELISA.
Results: The results of HBV markers test are presented in the table.

Group	n	HBsAg %	Anti-HBc %	Anti-HBs %
1	44	6.8	34.1	34.1
2	111	5.4	27.9	27.0
3	71	7.0	21.1	22.5
4	91	3.3	6.6	14.3

The data in the table show that, the exposure ofHBV infection in non vaccinated more than 20%, then vaccinated populations less than 7%.
Conclusion: The exposure and prevalence rate of HBV infection significant difference in vaccinated and non vaccinated population.

PP-120 Cloning and screening transregulated genes of HBEBP2 by SSH

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Objective: To screen and identify human genes transactivated by HBEBP2 by constructing a cDNA subtractive library with suppression subtractive hybridization (SSH) technique.
Methods: pcDNA3.1(–)-myc-his-HBEBP2 was constructed. Then the L02 cells was transfected by pcDNA3.1(–)-myc-his-HBEBP2 and pcDNA3.1(–)-myc-his empty vector, and SSH method was employed to analyze the differentially expressed DNA sequence between the two groups. After restriction enzyme *Rsa* I digestion, small sizes cDNAs were obtained. Then tester cDNA was divided into two groups and ligated to the specific adaptor 1 and adaptor 2, respectively. Aftertester cDNA was hybridized with driver cDNA twice and underwent two times of nested PCR, the second PCR production was subcloned into pGEM-Teasy plasmid vectors to set up the subtractive library. Amplification of the library was transformed into *E. coli*. The cDNA was sequenced and analyzed in GenBank with Blastn search after PCR.
Results: The subtractive library of genes transactivated by HBEBP2 was constructed successfully. The amplified library contains 80 positive clones containing 200 bp-1000 bp inserts. Sequence analysis was performed in 26 clones randomly, and the full length sequences were obtained with bioinformatics method. Altogether 7coding sequences were gotten.
Conclusions: The obtained sequences may be target genes transactivated by HBEBP2, and some genes coding proteins involved in metabolism, autoimmunity regulation, protein modification, cell cycle regulation.

PP-121 Construction and expression of a novel HBeAg binding protein 1 of hepatitis B virus in yeast

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Objective: To construct the eukaryotic expression vector of HBEBP1 gene and express HBEBP1 recombinant protein in yeast.
Methods: PCR was performed to amplify the gene of HBEBP1 from the cDNA template origining from HepG2, and the gene was cloned into pGEM-T vector. After sequencing, the correct DNA fragment was cut from pGEM-T-HBEBP1 and inserted into yeast expression plasmid pGBKT7. The reconstructed plasmid pGBKT7-HBEBP1 was transformed into yeast cell AH109 and screened on the synthetic dropout nutrient medium (SD/-Trp/Kana). The yeast protein was isolated and analyzed with SDS-PAGE and Western blot.
Results: The eukaryotic expressive vector was constructed successfully. The results of Western blot showed HBEBP1 protein was existed within yeast cells and the molecular weight of it was about 32.3kD.
Conclusions: The successful expression of HBEBP1 protein in yeast cells lay the foundation for studying biological function of HBEBP1.

PP-122 Association between IRF-3 polymorphisms and susceptibility to chronic hepatitis B virus infection

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Aim: To investigate the association between the three tagSNPs (rs10415576, rs2304204, rs2304206) of IRF3 gene and genetic susceptibility of chronic hepatitis B virus (HBV) infection in Chinese patients.
Materials and Methods: Based on the case-control study in 985 case of chronic HBV infection and 294 self-limiting HBV infection individuals as controls, three tagSNPs in the IRF3 gene were genotyped by Multiplex Snapshot technique. The genotype and allele frequencies were calculated and analyzed.
Results: The three SNPs sites showed no significant genotyping/allelic associations with chronic HBV infection. Overall allelic P values: rs10415576, $P = 0.0908$, OR (95%CI) = 1.1798 (0.9740–1.4291); rs2304204, $P = 0.5959$, OR (95%CI) = 1.0597 (0.8552–1.3133); rs2304206, $P = 0.8372$, OR (95%CI) = 1.0250 (0.8097–1.2976). Overall genotype P values: rs10415576, $P = 0.2106$; rs2304204, $P = 0.8458$; rs2304206, $P = 0.8315$. There was no statistically significant difference between chronic HBV infection and controls. Haplotypes generated by these three SNPs did not show significantly difference between the two groups either ($P > 0.05$).
Conclusion: The data suggest that the three tagSNPs sites of IRF3 gene are not associated with HBV infection in Chinese Han population.

PP-123 The role of HBeAg in the expression of B7-H1 on monocytes and IFN-γ in T cells

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Objective: To study the relationship between HBeAg and persistence of HBV infection.
Methods: Taking HBeAg negative CHB patients as the research objects, determined the expression of B7-H1/PD-1 and TLR-2 on $CD14^+$ PBMCs and IFN-γ and IL-4 in $CD3^+CD4^+$ cells before and after incubation with HBeAg and TLR-2